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EXAMINER	
DUNSTON, JENNIFER ANN	
ART UNIT	**PAPER NUMBER**
1636	

DATE MAILED: 11/01/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/705,757	WEIHE ET AL.	
	Examiner	Art Unit	
	Jennifer Dunston	1636	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *18 August 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-16,19-21,26-28,32-36,40,43,46,47,53,57 and 64* is/are pending in the application.

4a) Of the above claim(s) *16,19-21,26-28,35,36,40,43,46,53,57 and 64* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-15,32-34 and 47* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *12 November 0203* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *11/2/2004*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *Sequence Alignments*.

DETAILED ACTION

Receipt is acknowledged of an amendment, filed 4/21/2004, in which claims 17-18, 22-25, 29-31, 37-39, 41-42, 44-45, 48-52, 54-56, 58-63 and 65-82 were canceled.

Election/Restrictions

Applicant's election with traverse of Group I, the sequences of PIM-1 kinase (SEQ ID NOS: 1-6), and the polynucleotides and cells of claim 36[a-c, f9a-d)] in the reply filed on 8/18/2005 is acknowledged.

The traversal of the restriction of claim 47 is on the ground(s) that the steps of the method of claim 47 do not change depending upon which active ingredient is used, and that the search of the method to the full breadth of all active ingredients recited in claim 36 would not present any undue search burden. This is not found persuasive because the method steps of claim 47 do change depending upon the active ingredient used. The first positive action method step recited in claim 47 is "incubating a test substance with the active ingredient of claim 36". Thus, one must first provide the active ingredient of claim 36 in order to contact the active ingredient with the test substance. As indicated on pages 3-4 of the Office action mailed 7/14/2005, the polynucleotides and cells, proteins, and antibodies of claim 36 are biologically and functionally distinct from each other in that the each product is not needed to produce any other product. Based upon the distinct products encompassed by claim 36, one would have to use different methods of measuring binding of the test substance or measuring a functional parameter. For example, one could use reporter gene expression as a measure of binding in a cell, whereas a product such as an antibody would require a different binding assay. Therefore, the search of the

method for each distinct "active ingredient of claim 36" would not be coextensive, and the additional searching required would impose a serious search burden.

The traversal of the restriction between the different kinases is on the ground(s) that all compounds share a common utility and similar binding activity, which is likely the result of a common structure. This is not found persuasive because different structures may be capable of binding to the same compound. For example, the different PIM proteins may bind different structures within the same compound. Alternatively, the different PIM proteins may recognize the same structure by making different contacts with the compound. Further, PIM-1 is known to be capable of binding and phosphorylating different targets as compared to PIM-2 and PIM-3 (Bachmann et al, The International Journal of Biochemistry & Cell Biology, Vol. 37, pages 726-730, 2005; e.g. Abstract).

The requirement is still deemed proper and is therefore made FINAL.

Claims 16, 19-21, 26-28, 35-36, 40, 43, 46, 53, 57 and 64 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 8/18/2005. An examination of claims 1-15, 32-34 and 47 as they read on the elected invention follows.

Priority

Acknowledgment is made of applicant's claim for foreign priority under 35 U.S.C. 119(a)-(d). Receipt of the certified copy of the foreign priority document, Germany 101 23 055.9, is acknowledged. These papers have been placed of record in the file.

Information Disclosure Statement

Receipt of an information disclosure statement, filed on 11/2/2004, is acknowledged. The signed and initialed PTO 1449 has been mailed with this action.

Reference AI (Thomas R. Tolle, Chronischer Schmerz, 1997) was not considered because the reference is not in English and a concise explanation of relevance was not provided.

Specification

The disclosure is objected to because of the following informalities:

At page 40, line 2 of paragraph [00191], the name "Dubuisson" is misspelled.

At page 40, line 2 of paragraph [00191] and at page 49, paragraph [00228], the year of the Dubuisson reference is incorrect. The reference was published in 1977.

Appropriate correction is required.

Claim Objections

Claims 1-12, 32-34 and 47 are objected to because of the following informalities: the claims read on non-elected inventions. Correction is <u>not</u> required at this time.

Claim 32 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the

claim(s) in independent form. The claim is drawn to the use of a PIM1-, PIM2-, or PIM3-kinase in the method of claim 1. Claim 1 recites the use of a PIM1- or PIM-3 kinase. Therefore, claim 32 is broader in scope than claim 1.

Claim Rejections - 35 USC § 112

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-15 and 32-34 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 1 is vague and indefinite in that the metes and bounds of the claimed method are unclear. The preamble recites "a method for detecting a pain-regulating substance." However, it is not clear that measuring the binding of the test substance to a protein or part protein synthesized by the cell or measuring at least one functional parameter modified by the binding of the test substance to the protein or part protein will *necessarily* result in the identification of pain-regulating substances. The method steps encompass the testing of proteins defined by percent identity, hybridization and fragments of the elected PIM-1 kinase, yet the claims do not require that the proteins or part proteins encompassed by the claimed method have any particular functional activity. Further, any functional parameter may be modified, and it is not clear that any parameter will necessarily relate to the identification of pain-regulating substances. Therefore, it is unclear if one necessarily accomplishes what is intended for the method by practicing the recited method step(s). For the purposes of compact prosecution, the method of

claim 1 has been interpreted as a method of identifying pain-regulating substances (see the rejection under 35 USC 112, first paragraph) and has been interpreted as a method defined only by the recited method steps (see the rejections under 35 USC 102).

Claim 7 is vague and indefinite in that the metes and bounds of the phrase "which allow expression" are unclear. It is unclear if the phrase is referring to the protein or part protein of claim 1, or if another molecule is allowed to be expressed. For the purposes of examination, the phrase has been interpreted as allowing expression of the protein or part protein.

Claim 10 is vague and indefinite in that the metes and bounds of the phrase "via the activity bound thereto from a labeled test substance" are unclear. It is unclear as to how an "activity" can be bound to any protein or test substance. It is unclear if the activity of the PIM protein (e.g. kinase activity) is being measured in the presence of a labeled test substance. Alternatively, the "activity" could be binding itself, where the binding of the PIM protein to a labeled test substance is measured.

Claim 32 is vague and indefinite in that the metes and bounds of the phrase "in another part of the method the protein or part protein in steps (a) and (b)" in the 14th line of the claim are unclear. It is unclear to what "other part" of the method the claim is referring. Claim 32 depends from claim 1, which positively sets forth only two method steps, (a) and (b). Lines 4-13 of claim 32 set forth sequences that may be used in steps (a) and (b) of the method of claim 1. It is unclear if claim 32 is referring to steps not explicitly recited in claim 1 or if the claim is referring to a distinct method, wherein the protein or part protein in steps (a) and (b) is a PIM2- or PIM3-kinase. For the purposes of examination, the claim has been interpreted as referring to

PIM2- and PIM3-kinase sequences and variants thereof in the alternative as proteins or part proteins that may be used in the method of claim 1.

Claim 33 is vague and indefinite in that the metes and bounds of the phrase "in at least part of the method the protein or part protein in steps (a) and (b) is" are unclear. The phrase is unclear in that the only positive action method steps explicitly recited in the claims from which claim 33 depends are steps (a) and (b). It is unclear how one would accomplish the claimed method, if the protein were used only for part of the method (e.g. only in step (a) or only in step (b)). For the purposes of examination, the phrase has been interpreted as "wherein the protein or part protein of steps (a) and (b) is".

Claim 33 is vague and indefinite in that the metes and bounds of the phrase "in another part of the method the protein or part protein in steps (a) and (b)" in the 9th line of the claim are unclear. The preceding claims from which claim 33 depends (claims 1 and 32) positively set forth only two method steps, (a) and (b). Lines 3-8 of claim 33 set forth sequences that may be used in steps (a) and (b) of the method of claim 1. It is unclear if claim 33 is referring to steps not explicitly recited in claim 1 or if the claim is referring to a distinct method, wherein the protein or part protein in steps (a) and (b) is a PIM2- or PIM3-kinase. For the purposes of examination, the claim has been interpreted as referring to PIM2- and PIM3-kinase sequences and variants thereof in the alternative as proteins or part proteins that may be used in the method of claim 1.

Claim 34 is vague and indefinite in that the metes and bounds of the phrase "in at least part of the method the protein or part protein in steps (a) and (b) is" are unclear. The phrase is unclear in that the only positive action method steps explicitly recited in the claims from which

claim 34 depends are steps (a) and (b). It is unclear how one would accomplish the claimed method, if the protein were used only for part of the method (e.g. only in step (a) or only in step (b)). For the purposes of examination, the phrase has been interpreted as "wherein the protein or part protein of steps (a) and (b) is".

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 1-15 and 32-34 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

Enablement is considered in view of the Wands factors (MPEP 2164.01(A)). These include: nature of the invention, breadth of the claims, guidance of the specification, the existence of working examples, state of the art, predictability of the art and the amount of experimentation necessary. All of the Wands factors have been considered with regard to the instant claims, with the most relevant factors discussed below.

Nature of the invention: The claims are drawn to a method for detecting a pain-regulating substance. The positive action method steps require the provision of a cell or preparation from a cell which has synthesized a PIM1-kinase, a protein comprising the amino acid sequence of SEQ ID NO: 2, 4 or 6, a protein that is at least 90%, 95% or 97% homologous to a protein of SEQ ID NO: 2, 4 or 6, a protein encoded by a polynucleotide comprising the nucleic acid sequence of

SEQ ID NO: 1, 3 or 5, a protein encoded by a polynucleotide comprising a nucleic acid that is at least 90%, 95% or 97% homologous to a polynucleotide comprising the nucleic acid sequence of SEQ ID NO: 1, 3 or 5, a protein encoded by a nucleic acid that binds under stringent conditions to a polynucleotide comprising the nucleic acid sequence of SEQ ID NO: 1, 3 or 5 or antisense polynucleotides thereof, or a part protein of any of the abovementioned proteins that is at least 10 amino acids long. PIM1 kinase is a serine/threonine kinase. Other than PIM1 kinase, the amino acid sequences of SEQ ID NOS: 2, 4 and 6, and the proteins encoded by the nucleotide sequences of SEQ ID NOS: 1, 3 and 5, the proteins are defined by percent identity. The variants and fragments of PIM1 kinase encompassed by the claims are not required by the claims to have any particular functional activity. Step (a) of claim 1 requires the incubation of a test substance with a cell or preparation of a cell which has synthesized any of the abovementioned proteins or part proteins (hereinafter "protein or part protein"). Step (b) of claim 1 requires the measurement of binding of the test substance to the protein or part protein or the measurement of at least one functional parameter modified by the binding of the test substance to the protein or part protein.

The claimed methods utilize proteins encoded by nucleic acid molecules, wherein the nucleic acid sequence is defined only by percent identity to PIM-1. Further, the claimed methods encompass the use of proteins produced by cells containing nucleic acid sequences that encode PIM-1 "part proteins" of at least 10 amino acids. The sequences are not defined by any function. Although one could make the nucleic acid sequences and cells expressing the proteins defined only by sequence identity and length, one would not know how to use the sequences in an assay to detect pain-regulating substances.

The nature of the invention is complex in that the method is used to identify pain-regulating substances. The specification defines the term "pain-regulating" as relating to a potential regulating influence on the physiological pain event, in particular to an analgesic action or the substance directly or indirectly influences the perception of pain (e.g. paragraphs [0013] and [0021]). The claimed method encompass the identification of a pain-regulating substance as any substance that binds or does not bind to the protein or part protein. Further, the claimed methods encompass the use of any modulation of any function of the protein or part protein to determine if the test substance is a pain-regulating substance. Claims 11 and 12 further limit the step of measuring at least one functional parameter recited in the claims; however, the claims do not limit the direction of modulation (e.g. increased pH or decreased pH).

Breadth of the claims: The claims are broad in that a broad genus of proteins or part proteins is used in the claimed method. Further, the claims are broad in that they encompass any modification of binding of a test substance or any modification of the protein or part protein by the test substance as a method of detecting a pain-regulating substance. The complex nature of the subject matter of this invention is greatly exacerbated by the breadth of the claims.

Guidance of the specification and existence of working examples: The specification states that the starting point for the invention was "the identification of pain-regulated genes which are modified in either expression under pain conditions and are therefore probably involved, via their regulation connections, in the development and processing of chronic pain" (see paragraph [0007]). The specification envisions the interruption of the development of persistent pain, particularly chronic pain, by influencing the function of proteins that are formed to an increased or decreased extent in states of pain (e.g. paragraph [0008]). The specification asserts that PIM1-

and PIM3-kinase are regulated by pain or distributed in a pain-relevant manner, with PIM3-kinase having a pain-relevant distribution (e.g. paragraph [0016]). Based upon the modification of the expression or via the expression distribution in an *in vivo* pain model, the specification presumes the PIM1- and PIM3-kinases will have a "strong *in vivo* relevance" (e.g. paragraph [0017]).

Example 1 teaches the increase of PIM1 mRNA in the dorsal root ganglion (DRG) of animals injected with complete Freund's adjuvant (CFA), increase of PIM1 mRNA in the dorsal horn and motor neuron areas of the anterior horn after ischiadicus ligature of the rat, increase in PIM 1 in neuropathic pain regulation in microglia and neurons, and increase in PIM1 protein in the posterior horn in the Chung model (tight ligation and transection of the L(5) spinal nerve) (e.g. paragraphs [00217]-[00219]). Thus, Example 1 discloses the identification of PIM1 kinase as upregulated in pain.

Predictability and state of the art: Around the time the invention was made, PIM-1 protein was known to be a serine/threonine kinase with a role in tumorigenesis and cell survival in that PIM-1 kinase acts as to inhibit apoptosis and promote cell survival (Wang et al. J. Vet. Sci. Vol. 2, No. 3, pages 167-179, 2001; e.g. pages 167-170). Further, PIM-1 was known to play a role in hematopoiesis and germ cell maturation (Wang et al.; e.g. page 170). A more recent review of PIM-1 function indicates that PIM-1 binding partners have been identified, many of which are involved in the regulation of cell cycle progression and apoptosis (Bachmann et al. The International Journal of Biochemistry & Cell Biology, Vol. 37, pages 726-730, 2005; e.g. page 728, Biological Functions).

The increased expression of PIM-1 in pain models is correlative and does not necessarily indicate a role for PIM-1 kinase in the sensation of pain. Based upon the teachings discussed above, it is likely that PIM-2 kinase plays a role in apoptosis in the dorsal horn and dorsal root ganglion. At the time the invention was made, the role of apoptosis in neuropathic pain was underdeveloped. Whiteside et al (Journal of Neuroscience Research, Vol. 64, pages 168-173, 2001) teach that in the chronic constriction injury (CCI) model of neuropathic pain, a CCI to the sciatic nerve of adult rats results in an ipsilateral increase in apoptosis in the dorsal horn of the spinal cord (e.g. Abstract; page 168, paragraph bridging columns; page 170, paragraph bridging columns). However, Whiteside et al teach that the role of apoptosis in hyperalgesia is unclear (e.g. pages 170-172, Does Apoptosis Play a Role in Hyperalgesia?). Apoptosis may be a pathobiological mechanism of chronic pain. Alternatively, the neurons may be eliminated by apoptosis to enhance spinal sensitivity (Whiteside et al; e.g. paragraph bridging pages 171-172). Thus, it would be unpredictable to regulate pain through the regulation of apoptosis. Given the known role of PIM-1 in the prevention of apoptosis, the increased expression may be beneficial; the modulation of PIM-1 kinase may have an effect on cell survival without necessarily acting as an analgesic; or PIM-1 kinase may play a role in the pathobiology of hyperalgesia.

Amount of experimentation necessary: The quantity of experimentation necessary to carry out the claimed invention is high, as the skilled artisan could not rely on the prior art or the present specification to teach how to use the assay to identify a pain-regulating substance. In order to carry out the invention, it would be necessary for one to confirm that the PIM-1 kinase gene plays a role in pain. For example, one could treat pain model organisms with antisense oligonucleotides to PIM-1 kinase transcript. The reduction in pain observed in antisense treated

animals as compared to controls would provide a measure of confidence that one could identify pain-regulating substances. Next, one would have to identify the nucleic acid sequences defined by percent identity or length as compared to the nucleic acid sequence of PIM-1 kinase of human, mouse and rat (SEQ ID NOS: 1, 3 and 5) that are capable of functioning in a manner consistent with the detection of pain-regulating substances. Only when a role for PIM-1 in the pathobiology of pain has been confirmed and variant proteins and functional fragments of PIM-1 kinase have been identified, could one reasonably use the claimed method.

In view of the breadth of the claims and the lack of guidance provided by the specification as well as the unpredictability of the art, the skilled artisan would have required an undue amount of experimentation to make and/or use the claimed invention. Therefore, claims 1-15 and 32-34 are not considered to be enabled by the instant specification.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Claims 1-15, 32-34 and 47 are rejected under 35 U.S.C. 102(b) as being anticipated by Koike et al (FEBS Letters, Vol. 467, pages 17-21, 2000; see the entire reference) as evidenced by

Bachmann et al. (The International Journal of Biochemistry & Cell Biology, Vol. 37, pages 726-730, 2005; see the entire reference)

Regarding claims 1, 9 and 47, Koike et al teach plasmid pGLex-Pim-1Δ2, which contains an *Eco*RI-*Pst*I fragment of the human Pim-1 sequence of SEQ ID NO: 1 (see the attached alignment) (e.g. pages 17-18, section 2.2). Koike et al teach the transformation of *Sacharomyces cerevisiae* L40 cells with plasmid pGLex-Pim-1Δ2, and measuring the binding of the test substances, a HeLa MATCHMAKER cDNA library (e.g. page 18, section 2.3). Koike et al teach the measurement of binding by detecting LacZ reporter gene expression, a functional parameter modified by the binding of the test substance to the protein encoded by pGLex-Pim-1Δ2 (e.g. page 18, section 2.3).

Regarding claim 2, the *Sacharomyces cerevisiae* L40 cells are genetically modified with plasmid pGLex-Pim-1Δ2 prior to the incubation of the test substance (e.g. page 18, section 2.3).

Regarding claim 3, the genetic manipulation of the *Sacharomyces cerevisiae* L40 cells with plasmid pGLex-Pim-1Δ2 as taught by Koike et al allows the measurement of the LacZ expression (i.e. functional parameter) because L40 cells contain the LacZ reporter gene. Further, the *Sacharomyces cerevisiae* L40 cells have been genetically manipulated to contain the LacZ gene, which is not found in wild type *Sacharomyces cerevisiae*.

Regarding claim 4, the *Sacharomyces cerevisiae* L40 cells have been genetically modified with the LacZ gene such that LacZ gene expression can be used as a reporter of binding (e.g. page 18, section 3.2).

Regarding claim 7, Koike et al teach the culture of the *Sacharomyces cerevisiae* L40 cells transformed with plasmid pGLex-Pim-1Δ2 such that the Pim-1 fusion protein is expressed (e.g. page 18, section 3.1).

Regarding claim 8, the cells transformed with pGLex-Pim-1Δ2 and the cDNA library are cultured under selective pressure to identify colonies capable of growing on HIis- medium (e.g. page 18, section 3.1).

Regarding claims 11-12, Koike et al teach the measurement of binding by an activation of beta-galactosidase activity as a result of the modification of LacZ gene expression (e.g. page 18, section 2.3).

Regarding claims 5, 9, 13-15, 32-34 and 47, Koike et al teach the transfection of pCMV-FLAG-Pim-1 (containing a sequence consisting of SEQ ID NO: 1, which is 90% identical to SEQ ID NOS: 3 and 5, see the alignment) with pCMV-HP1-HA into human 293T cells (immortalized mammalian cells) and measurement of binding of Pim-1 and HP1 by immunoprecipitation (e.g. page 18, section 2.5). The percent identity between the human/mouse and human/rat proteins is evidenced by page 727, section 2 of Bachmann et al. Bachmann et al indicates that the mouse protein is 94% identical to the human protein, and the rat protein is 97% identical to the human protein.

Regarding claim 6, the nucleic acid sequence of Pim-1 is contained in the recombinant DNA construct of pCMV-FLAG-Pim-1 (e.g. page 18, section 2.5).

Regarding claim 10, the pCMV-HP1-HA plasmid encodes a test substance labeled with an HA tag, and the assay measures the binding of the test substance to the Pim-1 protein (e.g. page 18, section 2.5).

Claims 1-3, 5-7, 9-15, 32-34 and 47 are rejected under 35 U.S.C. 102(e) as being anticipated by Reinhard et al (US Patent Application Publication No. 2003/0045491; see the entire reference).

Regarding claims 1, 3, 5, 7, 10-15, 32-34 and 47, Reinhard et al teach TTK polynucleotides encoding TTK proteins such as PIM-1 (see the attached alignment). Reinhard et al teach that a TTK polypeptide may be produced using a cellular expression system (e.g. paragraphs [0106]-[0111] and [0138]). Reinhard et al teach screening assays to identify proteins or other substrates that bind to or modulate the action of a TTK protein (e.g. paragraphs [0119]-[0122]). Reinhard et al teach contacting one or more test substances with the polypeptide, testing the activity of the treated polypeptide (e.g. the ability to phosphorylate a substrate), and comparing that activity with the activity of the polypeptide in a comparable reaction medium untreated with the test substance(s) (e.g. paragraph [0132]). Reinhard et al exemplify an assay where a tagged fusion protein produced using a baculovirus expression system is mixed with a buffer, candidate agent, biotinylated substrate polypeptide (labeled ligand), and radioactively labeled ATP, and the activity of the TTK is measured by calculating the emission from the transferred radioactively labeled phosphate (e.g. paragraphs [0206]-[0207]).

Regarding claims 2 and 6, Reinhard et al teach the construction of polynucleotide constructs, for TTK expression in cells, using standard recombinant DNA techniques (e.g. paragraph [0107]).

Regarding claim 9, Reinhard et al teach the genetic manipulation and expression of the protein in a bacterial cell, yeast cell, insect cell or mammalian cell (e.g. paragraphs [0106]-[0111]).

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jennifer Dunston whose telephone number is 571-272-2916. The examiner can normally be reached on M-F, 9 am to 5 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Remy Yucel can be reached at 571-272-0781. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR, http://pair-direct.uspto.gov) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days.

Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Jennifer Dunston, Ph.D.
Examiner
Art Unit 1636

jad

TERRY MCKELVEY
PRIMARY EXAMINER

Qy = SEQ ID NO: 1

17	854	17.8	310	2	Q7ZVJ5	Q7zvj5 brachydanio
18	851	17.8	310	2	Q8JFW9	Q8jfw9 brachydanio
19	846	17.7	310	1	PIM1_BRARE	Q9yhz5 brachydanio
20	844	17.6	310	2	Q6DI52	Q6di52 brachydanio
21	724.5	15.1	221	2	Q8R1Z0	Q8r1z0 mus musculu
22	620	12.9	441	2	Q20443	Q20443 caenorhabdi
23	486	10.1	378	2	Q8T3F1	Q8t3f1 caenorhabdi
24	486	10.1	566	2	Q17737	Q17737 caenorhabdi
25	423	8.8	1383	1	PASK_MOUSE	Q8cee6 mus musculu
26	421.5	8.8	134	2	Q6P2J9	Q6p2j9 homo sapien
27	403	8.4	125	2	Q6Q2K5	Q6q2k5 canis famil
28	402	8.4	628	2	Q9H093	Q9h093 homo sapien
29	402	8.4	1398	2	O77268	O77268 drosophila
30	402	8.4	1398	2	Q9W532	Q9w532 drosophila
31	398	8.3	1107	2	Q6C310	Q6c310 yarrowia li
32	397	8.3	661	1	ARK5_HUMAN	O60285 homo sapien
33	393.5	8.2	832	2	Q963E6	Q963e6 drosophila
34	391.5	8.2	658	2	Q641K5	Q641k5 mus musculu
35	391.5	8.2	1033	2	Q8MLJ7	Q8mlj7 drosophila
36	391.5	8.2	1060	2	Q9V8W0	Q9v8w0 drosophila
37	391.5	8.2	1098	2	Q7KRK7	Q7krk7 drosophila
38	391.5	8.2	1138	2	Q7KRK3	Q7krk3 drosophila
39	390.5	8.2	631	2	Q8CIC0	Q8cic0 mus musculu
40	390.5	8.2	950	2	Q76N03	Q76n03 homo sapien
41	389	8.1	833	2	Q6NPA6	Q6npa6 drosophila
42	389	8.1	905	2	Q7KRK5	Q7krk5 drosophila
43	389	8.1	938	2	Q9V8V8	Q9v8v8 drosophila
44	389	8.1	1323	1	PASK_HUMAN	Q96rg2 homo sapien
45	388	8.1	1075	2	Q95U75	Q95u75 drosophila

ALIGNMENTS

3

RESULT 1
PIM1_HUMAN
ID PIM1_HUMAN STANDARD; PRT; 313 AA.
AC P11309; Q96RG3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37).
GN Name=PIM1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
RA Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
RT "Primary structure of the putative human oncogene, pim-1.";
RL Gene 90:303-307(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0;
RA Zakut-Houri R., Hazum S., Givol D., Telerman A.;
RT "The cDNA sequence and gene analysis of the human pim oncogene.";
RL Gene 54:105-111(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88217305; PubMed=3329709;
RA Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
RA Berns A.;
RT "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
RT and immunological identification of the in vitro synthesized PIM-1
RT protein.";
RL Oncogene Res. 1:103-112(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=88115604; PubMed=3429489;
RA Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
RT "Cloning and characterization of the human PIM-1 gene: a putative
RT oncogene related to the protein kinases.";

```
RL   J. Cell. Biochem. 35:105-112(1987).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 1-202 FROM N.A.
RX   MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
RA   Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA   Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
RT   "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT   cell lymphomas.";
RL   Nature 412:341-346(2001).
RN   [7]
RP   CHARACTERIZATION.
RX   MEDLINE=88246418; PubMed=2837645;
RA   Telerman A., Amson R., Zakut-Houri R., Givol D.;
RT   "Identification of the human pim-1 gene product as a 33-kilodalton
RT   cytoplasmic protein with tyrosine kinase activity.";
RL   Mol. Cell. Biol. 8:1498-1503(1988).
RN   [8]
RP   FUNCTION.
RX   MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4;
RA   Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.;
RT   "Identification of heterochromatin protein 1 (HP1) as a
RT   phosphorylation target by Pim-1 kinase and the effect of
RT   phosphorylation on the transcriptional repression function of
RT   HP1(1).";
RL   FEBS Lett. 467:17-21(2000).
RN   [9]
RP   SUBCELLULAR LOCATION.
RX   MEDLINE=22567470; PubMed=12680209;
RA   Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,
RA   Johnson T., Lilly M.B., Kraft A.S.;
RT   "Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
RT   localization is necessary for its biologic effects.";
RL   Anticancer Res. 23:167-178(2003).
CC   -!- FUNCTION: Thought to play a role in signal transduction in blood
CC       cells. May affect the structure or silencing of chromatin by
CC       phosphorylating HP1 gamma/CBX3.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC   -!- TISSUE SPECIFICITY: Expressed primarily in cells of the
CC       hematopoietic and germ line lineages.
CC   -!- PTM: Autophosphorylated on tyrosine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIM1ID261.html".
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M27903; AAA60090.1; -.
DR   EMBL; M16750; AAA60089.1; -.
DR   EMBL; M54915; AAA36447.1; -.
DR   EMBL; M24779; AAA81553.1; -.
DR   EMBL; BC020224; AAH20224.1; -.
DR   EMBL; AF386792; AAK70871.1; -.
DR   PIR; JU0327; TVHUP1.
DR   Genew; HGNC:8986; PIM1.
DR   H-InvDB; HIX0005835; -.
DR   MIM; 164960; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR   GO; GO:0007275; P:development; TAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Nuclear protein; Phosphorylation; Proto-oncogene;
KW   Serine/threonine-protein kinase; Transferase.
FT   DOMAIN       38    290       Protein kinase.
FT   NP_BIND      44     52       ATP (By similarity).
FT   BINDING      67     67       ATP (By similarity).
FT   ACT_SITE    167    167       Proton acceptor (By similarity).
FT   CONFLICT     15     16       AP -> RA (in Ref. 2).
SQ   SEQUENCE   313 AA;  35685 MW;  35BA76D3668E69A3 CRC64;

Alignment Scores:
Pred. No.:              5.43e-83        Length:         313
Score:                  1670.00         Matches:        313
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            34.87%          Indels:         0
DB:                     1               Gaps:           0

US-10-705-757-1 (1-2623) x PIM1_HUMAN (1-313)

Qy        351 ATGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCGCGCCCTGCAACGACCTG 410
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Db          1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20

Qy        411 CACGCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG 470
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Qy        471 GGCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGAC 530
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Db         41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60

Qy        531 AACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTG 590
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Db         61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80

Qy        591 CCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGTTTC 650
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Db         81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysLysValSerSerGlyPhe 100

Qy        651 TCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTG 710
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Db        101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120

Qy        711 GAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAAGGGGAGCCCTGCAA 770
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Db        121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140

Qy        771 GAGGAGCTGGCCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAAC 830
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Db        141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160

Qy        831 TGCGGGGTGCTACACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGC 890
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Db        161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180

Qy        891 GAGCTCAAGCTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACCGTCTACACGGAC 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200

Qy        951 TTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGC 1010
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Db        201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220

Qy       1011 AGGTCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATT 1070
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Db        221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240

Qy       1071 CCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCT 1130
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Db        241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260

Qy       1131 TCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACC 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280

Qy       1191 TTCGAAGAAATCCAGAACCATCCATGGATGCAAGATGTTCTCCTGCCCCAGGAAACTGCT 1250
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Db        281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300

Qy       1251 GAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA 1289
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Db        301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
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RESULT 2
PIM1_FELCA
ID   PIM1_FELCA     STANDARD;      PRT;   313 AA.
AC   Q95LJ0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
GN   Name=PIM1;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsujimoto H.;
RT   "The cDNA sequence of the feline pim-1 oncogene.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SUBUNIT: Binds to RP9 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC   -!- PTM: Autophosphorylated (By similarity).
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
CC       subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; AB073748; BAB71752.1; -.
DR   InterPro; IPR011009; Kinase_like.
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Qy = SEQ ID NO: 1


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Qy       1251 GAGATGGACCTCCACAGCCTGTCGCGGGGGCCCAGCAAA 1289
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Db        301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
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RESULT 2
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

Alignment Scores:

Pred. No.:	2.42e-94	Length:	313
Score:	1670.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.87%	Indels:	0
DB:	14	Gaps:	0

US-10-705-757-1 (1-2623) x US-10-081-119-18 (1-313)

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Qy        351 ATGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCGCGCCCTGCAACGACCTG 410
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Db          1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20

Qy        411 CACGCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40

Qy        471 GGCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGAC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60

Qy        531 AACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTG 590
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Db         61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80

Qy        591 CCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGTTTC 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysLysValSerSerGlyPhe 100

Qy        651 TCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120

Qy        711 GAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAAGGGGAGCCCTGCAA 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140

Qy        771 GAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAAC 830
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Db        141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160

Qy        831 TGCGGGGTGCTACACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGC 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180
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Qy        891 GAGCTCAAGCTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACCGTCTACACGGAC 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200

Qy        951 TTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGC 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220

Qy       1011 AGGTCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATT 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240

Qy       1071 CCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCT 1130
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Db        241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260

Qy       1131 TCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACC 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1191 TTCGAAGAAATCCAGAACCATCCATGGATGCAAGATGTTCTCCTGCCCCAGGAAACTGCT 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300

Qy       1251 GAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA 1289
              |||||||||||||||||||||||||||||||||||||||
Db        301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
```

RESULT 3
US-10-394-322A-52
; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT APPLICATION NUMBER: US/10/394,322A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-52

Alignment Scores:

Pred. No.:	2.42e-94	Length:	313
Score:	1670.00	Matches:	313
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	34.87%	Indels:	0
DB:	15	Gaps:	0

US-10-705-757-1 (1-2623) x US-10-394-322A-52 (1-313)

```
Qy        351 ATGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCGCGCCCTGCAACGACCTG 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20

Qy        411 CACGCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGTACCAGCTG 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40

Qy        471 GGCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGAC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60

Qy        531 AACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTG 590
```

Qy = SEQ ID NO:3

Db 301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 5
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Jefferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
; TITLE OF INVENTION: Target in Cancer
; FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-081-119-18

Alignment Scores:			
Pred. No.:	4.25e-109	Length:	313
Score:	1636.00	Matches:	304
Percent Similarity:	99.04%	Conservative:	6
Best Local Similarity:	97.12%	Mismatches:	3
Query Match:	66.97%	Indels:	0
DB:	14	Gaps:	0

US-10-705-757-3 (1-1302) x US-10-081-119-18 (1-313)

```
Qy          4 ATGCTCTTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCAGCCCCTTGCAACGACCTG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20

Qy         64 CACGCCAACAAGCTGGCGCCGGGCAAAGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG 123
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40

Qy        124 GGCCCGCTGTTGGGCAGCGGTGGCTTCGGCTCGGTCTACTCGGGCATCCGCGTCGCCGAC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||
Db         41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60

Qy        184 AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGAACTG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80

Qy        244 CCCAACGGCACCCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGCTTC 303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysLysValSerSerGlyPhe 100

Qy        304 TCGGGCGTCATTAGACTTCTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTG 363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120

Qy        364 GAGAGGCCCGAACCCGTGCAAGACCTCTTCGACTTCATCACCGAGCGAGGAGCCCTCCAG 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140

Qy        424 GAGGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGCCACAAC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160

Qy        484 TGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTGAACCGCGGC 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180

Qy        544 GAACTCAAACTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACAGTCTACACGGAC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200

Qy        604 TTTGACGGAACCCGAGTGTACAGTCCTCCAGAGTGGATTCGCTACCATCGCTACCACGGC 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220

Qy        664 AGGTCGGCTGCTGTTTGGTCCCTGGGGATCCTGCTCTATGACATGGTCTGCGGAGATATT 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240

Qy        724 CCATTTGAGCACGACGAAGAGATCGTCAAGGGCCAAGTGTACTTTAGGCAAAGGGTCTCT 783
              |||||||||||||||||||||||::::::||||||||:::|||||||||||||||||||
Db        241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260

Qy        784 TCAGAATGTCAACATCTTATTAGATGGTGCCTGTCCCTGAGACCATCGGACCGGCCCTCC 843
              |||||||||||||||||||||||||||||||:::|||||||||||||||||||||:::
Db        261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280

Qy        844 TTTGAAGAAATCCAGAACCATCCGTGGATGCAGGATGTTCTCCTGCCCCAGGCCACCGCC 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300

Qy        904 GAGATTCATCTGCACAGCCTGTCACCATCACCCAGCAAA 942
              |||||||||||||||||||||||||||   |||||||||
Db        301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
```

```
RESULT 6
US-10-394-322A-52
; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
;  APPLICANT: SUNESIS PHARMACEUTICALS, INC.
;  APPLICANT:  Prescott, John C.
;  TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
;  FILE REFERENCE: 39750-0006 US
;  CURRENT APPLICATION NUMBER: US/10/394,322A
;  CURRENT FILING DATE:  2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/366,892
;  PRIOR FILING DATE: 2002-03-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-394-322A-52

Alignment Scores:
Pred. No.:              4.25e-109      Length:          313
Score:                  1636.00        Matches:         304
Percent Similarity:     99.04%         Conservative:    6
Best Local Similarity:  97.12%         Mismatches:      3
Query Match:            66.97%         Indels:          0
DB:                     15             Gaps:            0

US-10-705-757-3 (1-1302) x US-10-394-322A-52 (1-313)

Qy          4 ATGCTCTTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCAGCCCCTTGCAACGACCTG 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20

Qy         64 CACGCCAACAAGCTGGCGCCGGGCAAAGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG 123
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40

Qy        124 GGCCCGCTGTTGGGCAGCGGTGGCTTCGGCTCGGTCTACTCGGGCATCCGCGTCGCCGAC 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db         41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60

Qy        184 AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGAACTG 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80
```

Qy = SEQ ID NO: 5

```
                 ||||||||||||:::||||||||||||||||||      |||||||||||        :::
Db         281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300

Qy         901 GAGATCGATCTGCACAGTCTGTCACCGGGATCCAGCAAG 939
               |||||||||||||||||||||||||||||||   ||||||
Db         301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313

RESULT 11
US-10-081-119-18
; Sequence 18, Application US/10081119
; Publication No. US20030045491A1
; GENERAL INFORMATION:
;  APPLICANT: Reinhard, Christoph
;  APPLICANT:  Jefferson, Anne B.
;  APPLICANT:  Chan, Vivien W.
;  TITLE OF INVENTION: TTK in Diagnosis and as a Therapeutic
;  TITLE OF INVENTION:  Target in Cancer
;  FILE REFERENCE: 16932.002
;  CURRENT APPLICATION NUMBER: US/10/081,119
;  CURRENT FILING DATE:  2002-02-21
;  PRIOR APPLICATION NUMBER: 60/289,813
;  PRIOR FILING DATE: 2001-02-21
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-081-119-18

Alignment Scores:
Pred. No.:                8.3e-111        Length:         313
Score:                    1582.00         Matches:        294
Percent Similarity:       97.12%          Conservative:   10
Best Local Similarity:    93.93%          Mismatches:     9
Query Match:              90.45%          Indels:         0
DB:                       14              Gaps:           0

US-10-705-757-5 (1-942) x US-10-081-119-18 (1-313)

Qy           1 ATGCTCCTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCCCGCCCCTGCAACGACCTG 60
               |||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db           1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20

Qy          61 CACGCCACCAAGCTGGCGCCGGGCAAAGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40

Qy         121 GGCCCGCTGTTGGGCAGCGGTGGCTTCGGCTCGGTCTACTCTGGCATCCGCGTCGCCGAC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db          41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60

Qy         181 AACTTGCCGGTGGCCATTAAGCACGTGGAGAAGGACCGGATTTCCGATTGGGGAGAACTG 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80

Qy         241 CCCAATGGCACCCGAGTGCCCATGGAAGTGGTCCTGTTGAAGAAGGTGAGCTCGGACTTC 300
               |||||||||||||||||||||||||||||||||||||||||||||||||||||    |||
Db          81 ProAsnGlyThrArgValProMetGluValValLeuLeuLysLysValSerSerGlyPhe 100

Qy         301 TCGGGCGTCATTAGACTTCTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         101 SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120

Qy         361 GAGAGGCCCGAACCGGTGCAAGACCTCTTCGACTTTATCACCGAACGAGGAGCCCTACAG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140

Qy         421 GAGGACCTGGCCCGAGGATTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGCCACAAC 480
               |||:::|||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db         141 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn 160

Qy         481 TGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTGAGCCGCGGC 540
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        161 CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly 180

Qy        541 GAAATCAAACTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACAGTCTACACGGAC 600
                 |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp 200

Qy        601 TTTGATGGGACCCGAGTGTACAGTCCTCCAGAGTGGATTCGCTACCATCGCTACCACGGC 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 PheAspGlyThrArgValTyrSerProProGluTrpIleArgTyrHisArgTyrHisGly 220

Qy        661 AGGTCGGCAGCTGTCTGGTCCCTTGGGATCCTGCTCTATGACATGGTCTGCGGAGATATT 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240

Qy        721 CCGTTTGAGCACGATGAAGAGATCATCAAGGGCCAAGTGTTCTTCAGGCAAACTGTCTCT 780
                 ||||||||||||||||||||||||||||:::||||||||||||||||||||||  ||||||
Db        241 ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260

Qy        781 TCAGAGTGTCAGCACCTTATTAAATGGTGCCTGTCCCTGAGACCGTCAGATCGGCCCTCC 840
                 ||||||||||||||||||||:::|||||||||:::|||||||||||||||||||||:::
Db        261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280

Qy        841 TTTGAAGAAATCCGGAACCATCCGTGGATGCAGGGTGACCTCCTGCCCCAGGCAGCTTCT 900
                 ||||||||||||:::|||||||||||||||||||  ||||||||||||      :::
Db        281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300

Qy        901 GAGATCCATCTGCACAGTCTGTCACCGGGATCCAGCAAG 939
                 ||||||||||||||||||||||||||||||||||  ||||||
Db        301 GluIleHisLeuHisSerLeuSerProGlyProSerLys 313
```

```
RESULT 12
US-10-394-322A-52
; Sequence 52, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
;  APPLICANT: SUNESIS PHARMACEUTICALS, INC.
;  APPLICANT:  Prescott, John C.
;  TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
;  FILE REFERENCE: 39750-0006 US
;  CURRENT APPLICATION NUMBER: US/10/394,322A
;  CURRENT FILING DATE:  2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/366,892
;  PRIOR FILING DATE: 2002-03-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 52
;   LENGTH: 313
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-394-322A-52

Alignment Scores:
Pred. No.:                8.3e-111      Length:          313
Score:                    1582.00       Matches:         294
Percent Similarity:       97.12%        Conservative:    10
Best Local Similarity:    93.93%        Mismatches:      9
Query Match:              90.45%        Indels:          0
DB:                       15            Gaps:            0

US-10-705-757-5 (1-942) x US-10-394-322A-52 (1-313)

Qy          1 ATGCTCCTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCCCGCCCCTGCAACGACCTG 60
                ||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db          1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu 20

Qy         61 CACGCCACCAAGCTGGCGCCGGGCAAAGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40

Qy        121 GGCCCGCTGTTGGGCAGCGGTGGCTTCGGCTCGGTCTACTCTGGCATCCGCGTCGCCGAC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||
Db         41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp 60
```